The nucleotide and predicted amino acid sequences of the cDNA clone PT4B (SEQ ID NO 8 and 9) obtained according to the sequencing strategy outlined in Figure 3B. Numbers shown above the amino acid sequence designate amino acid residue positions. The numbers on the right show nucleotide positions. All extracellular cysteines are marked by (•) or (o). The leader sequence (L), variable-like (v), joining-like (J), transmembrane TM, and cytplasmic (CYT) regions are indicated by horizontal arrows below the sequence, although the exact boundaries are ambiguous. Two Potential N-linked gylcosyltion sites (Asn-Leu-Thr) are also indicated (CHO).

Please replace the paragraphs on page 10, lines 12-33 with the following paragraph:

A. Alignment of the variable region amino acid sequence of T4 (SEQ ID NO 10) with a mouse kappa light chain immunoglobulin J606 (66) (SEQ ID NO 11), T8 (20) (SEQ ID NO. 13), a human T cell antigen receptor β-chain YT35 (97) (SEQ ID NO 14), and a human T cell antigen receptor -chain HPB-MLT (98) (SEQ ID NO 15). The invariant residues in the light chain variable region are included (Inv.) in the alignment (SEQ ID NO 12). The alignment was performed in order to maximize identities and structural homologies with T4, which appear as boxed residues. The lines below the sequence with letter A, B, C, C', D, E, F, and G indicate the residues which form β-strand G continues into the J sequence.

B. Alignment of the joining region amino acid sequence of T4 (SEQ ID NO 16) with the consensus J sequences of the T

cell antigen receptor β-chain (SEQ ID NO 17), immunoglobulin lambda (SEQ ID NO 18) and Kappa light chains (SEQ ID NO 19), and the J sequence of the human T cell receptor -chain (99) (SEQ ID NO 20).

C. Alignment of the transmembrane regions of T4 (SEQ ID NO 21) and an MHC class II β-chain (100) (SEQ ID NO 22). The putative transmembrane domain (TM) is indicated below the sequence.

Please replace the paragraph on page 16, lines 3-17 with the following paragraph:

This invention provides a therapeutic agent capable of specifically forming a complex with human immunodeficiency virus envelope glycoprotein comprising a poly-peptide. In one embodiment of the invention, the amino acid sequence of the polypeptide comprises the amino acid sequence shown in Figure 6 (SEQ ID NO 9) from about +1 to about +185 fused to the amino acid sequence from about +353 to about +371. In another embodiment of the invention, the amino acid sequence of the polypeptide comprises the amino acid sequence shown in Figure 6 (SEQ ID NO 9) from about +1 to about +106 fused to the amino acid sequence from about +353 to about +371. In yet a further embodiment of the invention, the amino acid sequence of the polypeptide comprises the amino acid sequence shown in Figure 6 (SEQ ID NO 9) from about +1 to about +185.

Please replace the paragraph on page 22, line 3 with the following paragraph:

The sequence of one sT4 (SEQ ID NO 1 and 2) is as follows:

Please replace the paragraph on page 95, lines 30-33 with the following paragraph:

5' -T ATG AAA AAG ACA GCT ATC GCG ATT GCA GTG GCA CTG GCT GGT TTC GCT ACC GTA GCG CAG GCC GGC TCT AGA GTC GAC CTA GTT AAC TAG-3' (SEQ ID NO 3)

Please replace the paragraph on page 96, lines 4-14 with the following paragraph:

Construction of OMPAST4BbvI: To create plasmid OMPAST4BbvI, plasmid OMPAST4 was cut with NaeI and XBaI. The smaller fragment resulting from this cut, containing the sT-4 coding region was deleted. Plasmid ST4BBVIDHFR was cut with KpnI and the resulting 3' overhang was blunt ended with T4 DNA polymerase. The blunt ended DNA was then cut with XBaI and the 1124 base pair fragment containing the nucleotides 145-1257 of the CT4 cDNA (SEQ ID NO 1) was isolated. The isolated fragment was ligated to the NaeI/Xbai cut OMPAST4 plasmid to create plasmid OMPASTI4BbVI.

Please replace the paragraph on page 96, lines 30-31 with the following paragraph:

5' gaccagaaggaggaggtgcaattgctagtgttcggattgactgccaac 3' (SEQ ID NO 4)
gtcttcctcctccacgttaacgatcacaagcctaactgacggttgagc 5' (SEQ ID NO 5)

Please replace the paragraph on page 97, lines 12-13 with the following paragraph:

Exhibit B

Please replace the paragraph on page 9, line 4-16 with the following paragraph:

The nucleotide and predicted amino acid sequences of the cDNA clone PT4B (SEQ ID NO 8 and 9) obtained according to the sequencing strategy outlined in Figure 3B. obtained according to the sequencing strategy outlined in Figure 3B. Numbers shown above the amino acid sequence designate amino acid residue positions. The numbers on the right show nucleotide positions. All extracellular cysteines are marked by (•) or (o). The leader sequence (L), variable-like (v), joining-like (J), transmembrane TM, and cytplasmic (CYT) regions are indicated by horizontal arrows below the sequence, although the exact boundaries are ambiguous. Two Potential N-linked gylcosyltion sites (Asn-Leu-Thr) are also indicated (CHO).

Please replace the paragraphs on page 10, lines 12-33 with the following paragraph:

A. Alignment of the variable region amino acid sequence of T4 (SEQ ID NO 10) with a mouse kappa light chain immunoglobulin J606 (66) (SEQ ID NO 11), T8 (20) (SEQ ID NO. 13), a human T cell antigen receptor β-chain YT35 (97) (SEQ ID NO 14), and a human T cell antigen receptor -chain HPB-MLT (98) (SEQ ID NO 15). The invariant residues in the light chain variable region are included (Inv.) in the alignment (SEQ ID NO 12). The alignment was performed in order to maximize identities and structural homologies with T4, which appear as boxed residues. The lines below the sequence with letter A, B, C, C', D, E, F, and G indicate the residues which form β-strand G continues into the J sequence.

B. Alignment of the joining region amino acid sequence of T4 (SEQ ID NO 16) with the consensus J sequences of the T cell antigen receptor β-chain (SEQ ID NO 17), immunoglobulin lambda (SEQ ID NO 18) and Kappa light chains (SEQ ID NO 19), and the J sequence of the human T cell receptor -chain (99) (SEQ ID NO 20).

C. Alignment of the transmembrane regions of T4 (SEQ ID NO 21) and an MHC class II β-chain (100) (SEQ ID NO 22). The putative transmembrane domain (TM) is indicated below the sequence.

Please replace the paragraph on page 16, lines 3-17 with the following paragraph:

This invention provides a therapeutic agent capable of specifically forming a complex with human immunodeficiency virus envelope glycoprotein comprising a poly-peptide. In one embodiment of the invention, the amino acid sequence of the polypeptide comprises the amino acid sequence shown in Figure 6 (SEQ ID NO 9) from about +1 to about +185 fused to the amino acid sequence from about +353 to about +371. In another embodiment of the invention, the amino acid sequence of the polypeptide comprises the amino acid sequence shown in Figure 6 (SEQ ID NO 9) from about +1 to about +106 fused to the amino acid sequence from about +353 to about +371. In yet a further embodiment of the invention, the amino acid sequence of the polypeptide comprises the amino acid sequence shown in Figure 6 (SEQ ID NO 9) from about +1 to about +185.

Please replace the paragraph on page 22, line 3 with the following paragraph:

The sequence of one sT4 (SEQ ID NO 1 and 2) is as follows:

Please replace the paragraph on page 95, lines 30-33 with the following paragraph:

5' -T ATG AAA AAG ACA GCT ATC GCG ATT GCA GTG GCA CTG GCT GGT TTC GCT ACC GTA GCG CAG GCC GGC TCT AGA GTC GAC CTA GTT AAC TAG-3' (SEQ ID NO 3)

Please replace the paragraph on page 96, lines 4-14 with the following paragraph:

Construction of OMPAST4BbvI: To create plasmid OMPAST4BbvI, plasmid OMPAST4 was cut with NaeI and XBaI. The smaller fragment resulting from this cut, containing the sT-4 coding region was deleted. Plasmid ST4BBVIDHFR was cut with KpnI and the resulting 3' overhang was blunt ended with T4 DNA polymerase. The blunt ended DNA was then cut with XBaI and the 1124 base pair fragment containing the nucleotides 145-1257 of the CT4 cDNA (SEQ ID NO 1) was isolated. The isolated fragment was ligated to the NaeI/Xbai cut OMPAST4 plasmid to create plasmid OMPASTI4BbVI.

Please replace the paragraph on page 96, lines 30-31 with the following paragraph:

5' gaccagaagggaggaggtgcaattgctagtggttcggattgactgccaac 3' (SEQ ID NO 4)
gtcttcctcctccacgttaacgatcacaagcctaactgacggttgagc 5' (SEQ ID NO 5)

Please replace the paragraph on page 97, lines 12-13 with the following paragraph:

5' gaccagaaggaggaggtgcaattgctagtgttcggattgactgccaac (SEQ ID NO 6)
gtcttcctcctccacgttaacgatcacaagcctaactgacggttgagc 5'(SEQ ID NO 7)